

Supplemental Table 1. Potential functional polymorphisms in nucleotide excision repair pathway genes as predicted by SNPinfo online software

rs	Chr	Allele	Position	TFBS	Splicing (ESE or ESS)	Splicing (abolish domain)	miRNA (miRanda)	miRNA (Sanger)	nsSNP	Polyphen	Reg Potential	Conservation	Nearby Gene	Distance (bp)	Allele	Asian	CHB	
rs2298881	19	A/C	50618756	Y	--	--	--	--	--	0.252611	0		ERCC1	14044 261	C	0.627	0.661	
rs3212986	19	C/A	50604576	--	--	--	--	--	Y	benign	0.305187	0		CD3EAP	3269 1288	C	0.617	0.685
rs11615	19	G/A	50615493	--	Y	--	--	--	--	0.26724	0.989		ERCC1	10781 3524	G	0.637	0.667	
rs1800975	9	T/C	99499399	Y	Y	--	--	--	--	0.483269	0		XPA	22387 113	C	0.592	0.644	
rs3176752	9	T/G	99477308	--	--	--	Y	Y	--	--	0.112079	0		XPA	296 22204	G	0.583	0.625
rs2228001	3	T/G	14162450	--	--	--	--	--	Y	--	0.189938	1		XPC	802 32693	T	0.610	0.685
rs2228000	3	G/A	14174889	--	--	--	--	--	Y	--	0.136701	0		XPC	13241 20254	G	0.617	0.685
rs2607775	3	C/G	14195099	Y	Y	--	--	--	--	0.282058	0		XPC	33451 44	C	0.624	0.696	
rs3810366	19	C/G	50565782	Y	--	--	--	--	--	0.174384	0		ERCC2 PPP1R13L	-113 -8954	C	0.611	0.685	
rs238406	19	G/T	50560149	--	Y	Y	--	--	--	0.36557	0.996		ERCC2	13463 5520	G	0.843	0.768	
rs13181	19	G/T	50546759	--	Y	Y	--	--	Y	benign	0.585468	0.999		ERCC2	73 18910	T	0.858	0.791
rs2276466	16	C/G	13950676	--	--	--	Y	Y	--	--	0.174235	0		ERCC4 MKL2	-971 -122021	C	0.838	0.768
rs2094258	13	T/C	102294760	Y	--	--	--	--	--	0	0.001		BIVM ERCC5	-2878 -1415	C	0.833	0.768	
rs751402	13	G/A	102296199	Y	Y	Y	--	--	--	0.25613	0		ERCC5	24 30147	G	0.838	0.789	
rs2296147	13	C/T	102296376	Y	--	--	--	--	--	0.175993	0		ERCC5	201 29970	T	0.856	0.768	
rs1047768	13	C/T	102302518	--	Y	Y	--	--	--	0.24405	0.914		ERCC5	6343 23828	T	0.844	0.774	
rs873601	13	A/G	102326338	--	Y	Y	Y	Y	--	--	0	0.005		ERCC5	30163 8	G	0.874	0.807